

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:44:30 ; Search time 816 Seconds  
(without alignments)  
780.321 Million cell updates/sec

Title: US-10-604-944A-14  
Perfect score: 77  
Sequence: 1 ttacccatagcgagaaca.....aactttaaatgcatgggttaa 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	77	8	US-10-604-944-14
2	77	100.0	845	3	US-09-756-551A-3
3	77	100.0	1092	5	US-10-003-035-34
4	77	100.0	1092	6	US-10-286-332A-34
5	77	100.0	1092	6	US-10-280-915-34
6	77	100.0	1092	8	US-10-286-332A-34
7	77	100.0	1092	8	US-10-280-915-34
8	77	100.0	1179	5	US-10-003-035-35
9	77	100.0	1179	6	US-10-286-332A-35
10	77	100.0	1179	6	US-10-280-915-35
11	77	100.0	1179	8	US-10-286-332A-35
12	77	100.0	1179	8	US-10-280-915-35
13	77	100.0	1308	5	US-10-003-035-36
14	77	100.0	1308	6	US-10-286-332A-36
15	77	100.0	1308	6	US-10-280-915-36
16	77	100.0	1308	8	US-10-286-332A-36
17	77	100.0	1308	8	US-10-280-915-36
18	77	100.0	1496	5	US-10-003-035-17
19	77	100.0	1496	6	US-10-286-332A-17
20	77	100.0	1496	6	US-10-280-915-17
21	77	100.0	1496	8	US-10-286-332A-17
22	77	100.0	1496	8	US-10-280-915-17
23	77	100.0	1503	3	US-09-968-355-25

24	77	100.0	1503	5	US-10-097-534-31	Sequence 31, Appl
25	77	100.0	1503	6	US-10-000-511A-9	Sequence 9, Appl
26	77	100.0	1503	6	US-10-000-511A-10	Sequence 10, Appl
27	77	100.0	1503	7	US-10-384-339C-138	Sequence 138, App
28	77	100.0	1503	8	US-10-844-658-8	Sequence 8, Appl
29	77	100.0	1515	6	US-10-102-622-5	Sequence 5, Appl
30	77	100.0	1548	3	US-09-968-355-19	Sequence 19, Appl
31	77	100.0	1596	3	US-09-968-355-22	Sequence 22, Appl
32	77	100.0	1621	3	US-09-882-945A-158	Sequence 158, App
33	77	100.0	1621	8	US-10-807-114-158	Sequence 158, App
34	77	100.0	1752	3	US-09-968-355-16	Sequence 16, Appl
35	77	100.0	1800	5	US-10-003-035-58	Sequence 58, Appl
36	77	100.0	1800	6	US-10-286-332A-58	Sequence 58, Appl
37	77	100.0	1800	6	US-10-280-915-58	Sequence 58, Appl
38	77	100.0	1800	8	US-10-286-332A-58	Sequence 58, Appl
39	77	100.0	1800	8	US-10-280-915-58	Sequence 58, Appl
40	77	100.0	2460	8	US-10-483-654-30	Sequence 30, Appl
41	77	100.0	3477	6	US-10-336-566-87	Sequence 87, Appl
42	77	100.0	3479	7	US-10-646-628-5	Sequence 5, Appl
43	77	100.0	3807	6	US-10-441-788-78	Sequence 78, Appl
44	77	100.0	4307	3	US-09-999-183-1	Sequence 1, Appl
45	77	100.0	4307	6	US-10-351-938-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-10-604-944-14  
; Sequence 14, Application US/10604944  
; Publication No. US20040219515A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICAL DETECTABLE GROUP OF NOVEL HIV REGULATORY GENES  
; FILE REFERENCE: 55008  
; CURRENT APPLICATION NUMBER: US/10/604,944  
; CURRENT FILING DATE: 2003-08-28  
; NUMBER OF SEQ ID NOS: 406  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14:  
; LENGTH: 77  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus 1  
US-10-604-944-14

Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.7e-18;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTACCTATAGTCGAGAACATCCAGGGCAATGTCATCATCAGGCCATATCACCTAGAAC	60
DB	1	TTACCTATAGTCGAGAACATCCAGGGCAATGTCATCATCAGGCCATATCACCTAGAAC	60
QY	61	TTTAAATGCAATGGGTAA	77
DB	61	TTTAAATGCAATGGGTAA	77

RESULT 2  
US-09-756-551A-3  
; Sequence 3, Application US/09756551A  
; Patent No. US20020051768A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Morrow et al.  
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL  
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 STATE STREET  
CITY: BOSTON

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:52:42 ; Search time 405 Seconds  
(without alignments)  
157.929 Million cell updates/sec

Title: US-10-604-944A-14  
Perfect score: 77  
Sequence: 1 ttacccttagtgagaaca.....aactttaaatgcatgggtaa 77

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New.\*  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
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10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	77	100.0	1515	7	US-10-507-928-5
2	77	100.0	1515	8	US-11-029-465-5
3	77	100.0	9719	10	US-11-042-988-10
4	75.4	97.9	1503	7	US-10-519-531-2
5	75.4	97.9	16360	7	US-10-519-531-1
6	75.4	97.9	17207	7	US-10-519-531-8
7	45.6	59.2	1521	8	US-11-129-442-22
8	44	57.1	1503	7	US-10-507-928-3
9	44	57.1	1503	8	US-11-029-465-3
10	44	57.1	1518	7	US-10-507-928-7
11	44	57.1	1518	8	US-11-029-465-7
12	42.4	55.1	1092	8	US-11-014-842A-40
13	42.4	55.1	5278	8	US-11-124-602-2
14	42.4	55.1	5304	8	US-11-124-602-1
15	28.2	36.6	1329	7	US-10-750-185-37952
16	28.2	36.6	1329	7	US-10-750-623-37952
17	26.4	34.3	1691140	8	US-11-091-018-1
18	25.8	33.5	697	7	US-10-750-185-28849
19	25.8	33.5	697	7	US-10-750-623-28849
20	24.8	32.2	98345	8	US-11-112-908-36
21	24.8	32.2	127340	8	US-11-112-908-35
22	24.4	31.7	1086	7	US-10-750-185-32559

C 23	24.4	31.7	1086	7	US-10-750-623-32559	Sequence 32559, A
C 24	24.2	31.4	28033	7	US-10-829-826B-42	Sequence 42, Appl
C 25	24.2	31.4	28033	7	US-10-829-826B-43	Sequence 43, Appl
C 26	23.8	30.9	643	8	US-11-043-753-1480	Sequence 1480, Ap
C 27	23.8	30.9	1280	7	US-10-750-185-53636	Sequence 53636, A
C 28	23.8	30.9	1280	7	US-10-750-623-53636	Sequence 53636, A
C 29	23.8	30.9	387780	7	US-10-995-561-13259	Sequence 13259, A
C 30	23.6	30.6	480	8	US-11-219-146-33	Sequence 33, Appl
C 31	23.6	30.6	480	8	US-11-219-146-35	Sequence 35, Appl
C 32	23.6	30.6	480	8	US-11-219-146-37	Sequence 37, Appl
C 33	23.6	30.6	480	8	US-11-219-146-39	Sequence 39, Appl
C 34	23.6	30.6	600	8	US-11-219-146-41	Sequence 41, Appl
C 35	23.6	30.6	600	8	US-11-219-146-43	Sequence 43, Appl
C 36	23.6	30.6	600	8	US-11-219-146-45	Sequence 45, Appl
C 37	23.6	30.6	600	8	US-11-219-146-47	Sequence 47, Appl
C 38	23.6	30.6	752	8	US-11-219-146-17	Sequence 17, Appl
C 39	23.6	30.6	752	8	US-11-219-146-19	Sequence 19, Appl
C 40	23.6	30.6	752	8	US-11-219-146-21	Sequence 21, Appl
C 41	23.6	30.6	752	8	US-11-219-146-23	Sequence 23, Appl
C 42	23.6	30.6	1151	8	US-11-219-146-1	Sequence 1, Appl
C 43	23.6	30.6	1151	8	US-11-219-146-3	Sequence 3, Appl
C 44	23.6	30.6	1151	8	US-11-219-146-5	Sequence 5, Appl
C 45	23.6	30.6	1151	8	US-11-219-146-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-10-507-928-5  
; Sequence 5, Application US/10507928  
; Publication No. US20050266024A1  
; GENERAL INFORMATION:  
; APPLICANT: POWDERED LIMITED AND GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ADJUVANT  
; FILE REFERENCE: N.88232B GCW  
; CURRENT APPLICATION NUMBER: US/10/507,928  
; CURRENT FILING DATE: 2004-09-17  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: nucleotide sequence of the p17/24trNEF insert in p17/24trNEF1  
US-10-507-928-5

Query Match	100.0%	Score 77;	DB 7;	Length 1515;
Best Local Similarity	100.0%	Pred. No. 4.3e-20;		
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Qy	1	TTACCTTATAGTCAGAACATCCAGGGCAATGTCATCAGGCCATATCACCTAGAAC	60	
Db	393	TTACCTTATAGTCAGAACATCCAGGGCAATGTCATCAGGCCATATCACCTAGAAC	452	
Qy	61	TTTAAATGTCATGGGTAA	77	
Db	453	TTTAAATGTCATGGGTAA	469	

RESULT 2  
US-11-029-465-5  
; Sequence 5, Application US/11029465  
; Publication No. US20050256070A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomsen, Ralph P.  
; APPLICANT: Braun, Ralph P.  
; APPLICANT: Thomsen, Lindy  
; APPLICANT: Van-Wely, Catherine  
; APPLICANT: Ertl, Peter  
; TITLE OF INVENTION: Adjuvant  
; FILE REFERENCE: 033267-015  
; CURRENT APPLICATION NUMBER: US/11/029,465

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:41:26 ; Search time 142 Seconds  
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963.889 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77

Sequence: 1 ttacctatagtcagaaca.....aactttaaatgcattggttaa 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/6 COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
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8: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	840	2	US-07-979-966A-1
2	77	100.0	845	2	US-08-589-446-3
3	77	100.0	845	2	US-08-444-882-3
4	77	100.0	845	2	US-08-389-459A-3
5	77	100.0	845	3	US-08-987-867A-3
6	77	100.0	1314	3	US-08-392-794A-1
7	77	100.0	2095	2	US-08-333-901-5
8	77	100.0	2095	2	US-08-456-582-5
9	77	100.0	2095	2	US-08-898-789-5
10	77	100.0	3807	2	US-08-417-210A-78
11	77	100.0	3807	3	US-09-136-159A-78
12	77	100.0	4307	3	US-09-552-950-1
13	77	100.0	4307	3	US-09-936-572-1
14	77	100.0	4338	3	US-09-872-733A-1
15	77	100.0	5362	3	US-08-463-210-5
16	77	100.0	5362	3	US-08-463-028-5
17	77	100.0	5362	3	US-08-463-209-5
18	77	100.0	7228	2	US-08-850-049-128
19	77	100.0	7228	2	US-08-850-049-129
20	77	100.0	7228	2	US-08-050-478-128
21	77	100.0	7228	2	US-08-050-478-129
22	77	100.0	7228	3	US-09-414-117-128
23	77	100.0	7228	3	US-09-414-117-129
24	77	100.0	7228	3	US-09-678-437-128

25	77	100.0	7228	3	US-09-678-437-129	Sequence 129, App
26	77	100.0	7228	3	US-09-943-722-128	Sequence 128, App
27	77	100.0	7228	3	US-09-943-722-129	Sequence 129, App
28	77	100.0	8366	3	US-09-872-733A-6	Sequence 6, Appli
29	77	100.0	8560	3	US-09-936-572-11	Sequence 11, Appli
30	77	100.0	8932	3	US-09-124-900-1	Sequence 1, Appli
31	77	100.0	8933	3	US-08-463-210-4	Sequence 4, Appli
32	77	100.0	8933	3	US-09-620-958A-3	Sequence 3, Appli
33	77	100.0	8933	3	US-09-620-958A-9	Sequence 4, Appli
34	77	100.0	8933	3	US-08-463-028-4	Sequence 9, Appli
35	77	100.0	8933	3	US-08-463-028-4	Sequence 4, Appli
36	77	100.0	8933	3	US-09-943-286-3	Sequence 3, Appli
37	77	100.0	8933	3	US-09-943-286-4	Sequence 4, Appli
38	77	100.0	8933	3	US-09-943-286-4	Sequence 3, Appli
39	77	100.0	8933	3	US-09-943-286-4	Sequence 3, Appli
40	77	100.0	9609	3	US-09-943-286-9	Sequence 3, Appli
41	77	100.0	9719	3	US-09-700-304-1	Sequence 4, Appli
42	75.4	97.9	1503	3	US-09-393-795-2	Sequence 1, Appli
43	75.4	97.9	7399	2	US-08-418-848A-9	Sequence 9, Appli
44	75.4	97.9	9709	2	US-08-188-583-5	Sequence 5, Appli
45	75.4	97.9	9709	3	US-08-388-353-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-07-979-966A-1  
; Sequence 1, Application US/07979966A  
; Patent No. 5707864  
; GENERAL INFORMATION:  
; APPLICANT: Myron E. Essex  
; APPLICANT: Xiaofang Yu  
; APPLICANT: Tun-Hou Lee  
; TITLE OF INVENTION: AIDS THERAPEUTICS BASED ON HIV  
; TITLE OF INVENTION: MA PEPTIDES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/979,966A  
; FILING DATE: No. 5707864ember 23, 1992  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: John W. Freeman  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 00379/018001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-979-966A-1

Query Match 100.0%; Score 77; DB 2; Length 840;